

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 22, 2004, 13:51:35 ; Search time 75.7714 Seconds
(without alignments)
1136.247 Million cell updates/sec

Title: US-10-630-406-8

Perfect score: 1244

Sequence: 1 MEAPQLFLLLMLPDTG.....EVTHQGLSSPVTKSFNRGEC 240

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- A_Geneseq 23Sep04:*
- 1: Geneseq1980s:*
 - 2: Geneseq1990s:*
 - 3: Geneseq2000s:*
 - 4: Geneseq2001s:*
 - 5: Geneseq2002s:*
 - 6: Geneseq2003as:*
 - 7: Geneseq2003bs:*
 - 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1244	100.0	240	ADJ65029	Adj65029 Plasmid p
2	1133	91.1	240	AAY50161	Aay50161 Human res
3	1128.5	90.7	241	AAR28809	Aar28809 Vector pM
4	1122	90.2	240	AAR27927	Aar27927 Human CC4
5	1122	90.2	240	ABR82836	ABR82836 Antibody
6	1099	88.3	240	AUJ00815	AuJ00815 Human Imm
7	1075	86.4	244	AAI96305	Aai96305 Human IGF
8	1066	85.7	220	ADK52334	Adk52334 Human ant
9	1063	85.5	238	ADL23055	Adl23055 Humanised
10	1061	85.3	220	ADK52386	Adk52386 Human ant
11	1059	85.1	240	AAY50156	Aay50156 Chimeric
12	1057	85.0	220	ADK52362	Adk52362 Human ant
13	1056	84.9	220	ADK52314	Adk52314 Human ant
14	1053	84.6	238	ADA47330	Ada47330 TRX1 high
15	1053	84.6	238	ADA47332	Ada47332 TRX1 high
16	1053	84.6	238	ADP88450	Adp88450 Antibody
17	1053	84.6	238	ADP88426	Adp88426 Antibody
18	1052.5	84.6	235	AAV93702	Aav93702 The kappa
19	1052.5	84.6	235	AAV93729	Aav93729 The kappa
20	1052.5	84.6	235	AAE35884	Aae35884 Human 4.1
21	1051	84.5	234	AAI92239	Aai92239 Human bon
22	1047	84.2	220	ADK52298	Adk52298 Human ant
23	1043.5	83.9	235	ABP71366	Abp71366 Anti-OPGL
24	1043	83.8	238	ADA47339	Ada47339 TRX1 high
25	1043	83.8	238	ADA47338	Ada47338 TRX1 high

26	1043	83.8	238	ADP88434	Adp88434 Antibody
27	1043	83.8	238	ADP88442	Adp88442 Antibody
28	1041	83.7	220	AAV08601	Aav08601 JP1112785
29	1040.5	83.6	233	AAV93704	Aav93704 The kappa
30	1040.5	83.6	233	AAV93731	Aav93731 The kappa
31	1040.5	83.6	233	AAE35886	Aae35886 Human 4.8
32	1037	83.4	234	AAV93733	Aav93733 The kappa
33	1037	83.4	234	AAV93708	Aav93708 The kappa
34	1037	83.4	234	AAE35888	Aae35888 Human 6.1
35	1036	83.3	234	ADK28481	Adk28481 Human ant
36	1036	83.3	236	AAU74299	Aau74299 Anti-huma
37	1032.5	83.0	239	ADK70470	Adk70470 Respirato
38	1032	83.0	234	AAE52951	Aae52951 Human ant
39	1031.5	82.9	235	ADM41573	Adm41573 Anti-ince
40	1030	82.8	236	AAG71272	Aag71272 Human gen
41	1030	82.8	236	ABG63490	Abg63490 Human alb
42	1030	82.8	236	ADL76755	Adl76755 Albumin f
43	1029.5	82.8	237	AAW73873	Aaw73873 Human ant
44	1028	82.6	236	AAU74301	Aau74301 Anti-huma
45	1027	82.6	242	AAU80338	Aau80338 Human mil

ALIGNMENTS

RESULT 1

ADJ65029
ID ADJ65029 standard; protein; 240 AA.

XX AC ADJ65029;

XX AC (first entry)

XX 06-MAY-2004 (first entry)

XX Plasmid pD16-H39E3.L1 light chain antibody amino acid sequence SEQ:8.

XX humanised antibody; human 4-1BB; human 4-1BB ligand; cancer; cytostatic;

XX gene therapy; antibody; plasmid; pD16-H39E3.L1.

XX Synthetic.

XX W02004010947-A2.

XX 05-FEB-2004.

XX 30-JUL-2003; 2003WO-US023735.

XX 30-JUL-2002; 2002US-0399646P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX Jure-Kunkel M, Ganguly S, Abraham R, Hollenbaugh DL, Rillema J;

XX Thorne B, Shuford WW, Mittler RS;

XX WPI; 2004-143726/14.

XX N-PSDB; ADJ65027.

XX New humanized antibody that binds to human 4-1BB and allows binding of human 4-1BB to a human 4-1BB ligand, useful for preparing a composition for treating cancer.

XX Claim 4; SEQ ID NO 8; 78pp; English.

XX The present invention describes a humanised antibody (I) that binds to human 4-1BB and allows binding of human 4-1BB to a human 4-1BB ligand.

XX (Also described: (1) a pharmaceutical composition comprising the antibody (I) and a carrier; (2) treating cancer in a subject; and (3) an isolated polynucleotide comprising nucleotides 693-2072 of the 7033-base pairs

XX (bp) sequence (SEQ ID NO: 3, ADJ65024) or nucleotides 633-1034 or 1409-1726 of the 8874-bp sequence (SEQ ID NO: 6, ADJ65027). (I) has cytostatic activity, and can be used in gene therapy. The humanised antibody (I) can be used for preparing a composition for treating cancer. The present

XX sequence represents the plasmid pD16-H39E3.L1 light chain antibody amino acid sequence, which is used in an example from the present invention.

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XX SQ Sequence 240 AA;
Query Match 100.0%; Score 1244; DB 8; Length 240;
Best Local Similarity 100.0%; Pred. No. 3.9e-68;
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEAPAQQLFLLLLWLPDTTGDIVNTQSPDSLAVSLGERATINCKSSQSLSSGNQKQVLA 60
Db 1 MEAPAQQLFLLLLWLPDTTGDIVNTQSPDSLAVSLGERATINCKSSQSLSSGNQKQVLA 60

Qy 61 WYQKPGQPKLIYVASTQSGVDPFRFGSGSGTDTFTLTISLQAEADVAVVYCLQYDRY 120
Db 61 WYQKPGQPKLIYVASTQSGVDPFRFGSGSGTDTFTLTISLQAEADVAVVYCLQYDRY 120

Qy 121 PFTFGQGTKLEIKETVAAPSVFIPPSDEOLKSGTASVCLLNFPYPRAKVQWKVDNAL 180
Db 121 PFTFGQGTKLEIKETVAAPSVFIPPSDEOLKSGTASVCLLNFPYPRAKVQWKVDNAL 180

Qy 181 QSGNSQSVTEQDSKSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db 181 QSGNSQSVTEQDSKSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240

RESULT 2
ID AAY50161 standard; protein; 240 AA.
XX AC AAY50161;
XX DT 17-OCT-2003 (revised)
XX DT 31-JAN-2000 (first entry)
XX DE Human reshaped F19 antibody light chain (version a).

KW Antibody; monoclonal; F19; fibrinogen activation protein alpha; PAP;
KW humanisation; complementarity determining region; CDR; CDR grafting;
KW reshaped; reactive stroma; fibroblast; epithelial cancer; diagnosis;
KW immune response; framework sequence; constant region; variable region;
KW producibility; treatment; cancer; colorectal; lung; breast; head; neck;
KW ovarian; lung; bladder; pancreatic; metastasis; detection; wound healing;
KW skin inflammation; tumour; immunogenicity; chimeric; light chain.

XX Mus sp.
XX OS Homo Sapiens.
XX OS Chimeric.

XX FH Key
XX FT Peptide 1..20
XX FT Protein 21..240
XX FT Region 21..140
XX FT /note= "Mature human reshaped F19 light chain"
XX FT /note= "Mature reshaped human F19 light chain variable region"
XX FT Region 44..60
XX FT /note= "Complementarity determining region (CDR) 1"
XX FT Region 76..82
XX FT /note= "CDR 2"
XX FT Region 115..123
XX FT /note= "CDR 3"
XX FT Region 141..240
XX FT /note= "Human kappa light chain constant region"

XX EP953639-A1.
XX XX
XX DD 03-NOV-1999.
XX EF 30-APR-1998; 98EP-00107925.
XX PR 30-APR-1998; 98EP-00107925.
XX XX
XX PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.

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XX PI Park JE, Garin-Chesa P, Bamberger U, Leger O, Saldanha J;
XX RT Rettig WJ;
XX WPI; 1999-621833/54.
XX DR N-PSDB; AAZ32784.
XX PT New antibody protein, useful for treating cancer and for imaging presence
XX of activated stromal fibroblasts in healing wound or inflamed skin.
XX PS Example 3; Fig 30; 143pp; English.
XX CC This sequence represents the light chain (version a) of a reshaped human
XX F19 antibody. F19 (ATCC Accession number HB 8269) is a murine monoclonal
XX antibody against fibroblast activation protein alpha (FAP). FAP is a cell
XX surface molecule of reactive stromal fibroblasts, and its induction is a
XX highly consistent molecular trait of the reactive stroma of many types of
XX epithelial cancer. Although F19 may be useful in vitro, e.g., for
XX diagnosis, its applications for in vivo use in humans are problematic as
XX it elicits a human anti-mouse response which reduces the efficacy of the
XX antibody in patients and impairs continued administration. The novel
XX human reshaped F19 was humanised by grafting the murine complementarity
XX determining regions (CDRs) of F19 onto human variable region framework
XX sequences, and then joining these "reshaped human" variable regions to
XX human constant regions. These modifications also result in the improved
XX producibility in eukaryotic cell culture systems as compared to a
XX chimeric antibody having the entire variable regions of F19 joined to
XX human constant regions. The human reshaped F19 antibody has low
XX immunogenicity for humans and is useful for treating cancers e.g.,
XX colorectal cancers, non-small cell lung cancers, breast cancers, head and
XX neck cancers, ovarian cancers, lung cancers, bladder cancers, pancreatic
XX cancers and metastatic cancers. It is also useful for the detection of
XX activated stromal fibroblasts in a healing wound, inflamed skin or a
XX tumour in a human patient. (Updated on 17-OCT-2003 to standardise OS
XX field)
XX SQ Sequence 240 AA;

Query Match 91.1%; Score 1133; DB 2; Length 240;
Best Local Similarity 91.2%; Pred. No. 2.1e-61;
Matches 219; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MEAPAQQLFLLLLWLPDTTGDIVNTQSPDSLAVSLGERATINCKSSQSLSSGNQKQVLA 60
Db 1 METDTLLWLLWVPGSSGDIWNTQSPDSLAVSLGERATINCKSSQSLSSGNQKQVLA 60

Qy 61 WYQKPGQPKLIYVASTQSGVDPFRFGSGSGTDTFTLTISLQAEADVAVVYCLQYDRY 120
Db 61 WYQKPGQPKLIYVASTQSGVDPFRFGSGSGTDTFTLTISLQAEADVAVVYCLQYDRY 120

Qy 121 PFTFGQGTKLEIKETVAAPSVFIPPSDEOLKSGTASVCLLNFPYPRAKVQWKVDNAL 180
Db 121 PLTFGQGTKEIKETVAAPSVFIPPSDEOLKSGTASVCLLNFPYPRAKVQWKVDNAL 180

Qy 181 QSGNSQSVTEQDSKSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db 181 QSGNSQSVTEQDSKSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240

RESULT 3
AAR28809
ID AAR28809 standard; protein; 241 AA.
XX AC AAR28809;
XX DT 25-MAR-2003 (revised)
XX DT 02-APR-1993 (first entry)
XX DE Vector pMDR1007.
XX KW Plasmid; pMDR1006; pSAB132; vector; pMDR1007; pMDR985; AatII; EcoRV;
XX pMDR986; BglII; pMDR1003; JA221(Iq); E. coli; ampicillin resistance;
XX NotI; dephosphorylate; calf; alkaline phosphatase; low temperature;

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OM protein - protein search, using sw model

Run on: November 22, 2004, 14:02:36 ; Search time 128.143 Seconds

(without alignments)
1271.227 Million cell updates/sec

Title: US-10-630-406-5

Perfect score: 2454

Sequence: 1 MDWTWRIFLVAAATGAHSE.....MHEALHNHYTKSLISLQK 460

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2454	100.0	460	16	US-10-630-406-5
2	2269	92.5	462	16	Sequence 5, Appl1
3	2268.5	92.4	463	16	Sequence 163, App
4	2267.5	92.4	469	16	Sequence 160, App
5	2267	92.4	462	16	Sequence 164, App
6	2266	92.3	465	16	Sequence 155, App
7	2262.5	92.2	469	16	Sequence 162, App
8	2262	92.2	464	16	Sequence 157, App
9	2261	92.1	468	16	Sequence 158, App
10	2260	92.1	462	16	Sequence 161, App
11	2256	91.9	464	16	Sequence 165, App
12	2255	91.9	460	16	Sequence 156, App
13	2222.5	90.6	465	14	Sequence 159, App

14	2205	89.9	443	9	US-09-917-410-4	Sequence 4, Appl1
15	2196	89.5	466	15	US-10-656-769-30	Sequence 30, Appl1
16	2190	89.2	466	15	US-10-656-769-34	Sequence 24, Appl1
17	2113	86.1	468	15	US-10-377-109-2	Sequence 2, Appl1
18	2106.5	85.8	467	14	US-10-428-408A-30	Sequence 30, Appl1
19	2106.5	85.8	467	15	US-10-428-894-30	Sequence 30, Appl1
20	2106.5	85.8	467	17	US-10-693-874-30	Sequence 30, Appl1
21	2100.5	85.6	473	15	US-10-038-591-50	Sequence 50, Appl1
22	2100.5	85.6	473	17	US-10-775-444A-50	Sequence 50, Appl1
23	2098	85.5	470	15	US-10-038-591-49	Sequence 49, Appl1
24	2098	85.5	470	17	US-10-775-444A-49	Sequence 49, Appl1
25	2097.5	85.5	467	15	US-10-180-648-2	Sequence 2, Appl1
26	2093	85.3	464	15	US-10-032-037B-26	Sequence 26, Appl1
27	2093	85.3	464	15	US-10-029-988B-26	Sequence 26, Appl1
28	2093	85.3	464	15	US-10-032-433A-26	Sequence 26, Appl1
29	2093	85.3	464	15	US-10-029-926B-26	Sequence 26, Appl1
30	2090	85.2	470	15	US-10-038-591-46	Sequence 46, Appl1
31	2090	85.2	470	17	US-10-775-444A-46	Sequence 46, Appl1
32	2081.5	84.8	469	14	US-10-292-088-54	Sequence 54, Appl1
33	2079	84.7	470	15	US-10-038-591-45	Sequence 45, Appl1
34	2079	84.7	470	17	US-10-775-444A-45	Sequence 45, Appl1
35	2078.5	84.7	465	15	US-10-656-769-28	Sequence 28, Appl1
36	2077.5	84.7	444	14	US-10-150-475A-6	Sequence 6, Appl1
37	2077.5	84.7	444	16	US-10-704-522-6	Sequence 6, Appl1
38	2077.5	84.7	444	16	US-10-645-215-6	Sequence 3, Appl1
39	2077	84.6	474	10	US-09-848-832-3	Sequence 3, Appl1
40	2077	84.6	474	14	US-10-225-108A-3	Sequence 1, Appl1
41	2077	84.6	474	15	US-10-461-148-1	Sequence 13, Appl1
42	2074.5	84.5	463	14	US-10-153-382-13	Sequence 39, App
43	2074.5	84.5	477	14	US-10-291-255-395	Sequence 33, Appl1
44	2073.5	84.5	4852	15	US-10-412-406-33	Sequence 9, Appl1
45	2073	84.5	464	14	US-10-153-382-9	

ALIGNMENTS

RESULT 1
US-10-630-406-5
; Sequence 5, Application US/10630406
; Publication No. US20040105855A1
; GENERAL INFORMATION:
; APPLICANT: Jure-Kunkel, Maria
; APPLICANT: Ganguly, Subiray
; APPLICANT: Abraham, Ralph
; APPLICANT: Hollenbaugh, Diane L.
; APPLICANT: Rillema, Jill
; APPLICANT: Thorne, Barbara
; APPLICANT: Shuford, Walter W.
; APPLICANT: Mittler, Robert S.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN 4-1BB
; FILE REFERENCE: D0288 NP
; CURRENT APPLICATION NUMBER: US/10/630,406
; CURRENT FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/399,646
; PRIOR FILING DATE: 2002-07-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-630-406-5

Query Match 100.0%; Score 2454; DB 16; Length 460;
Best Local Similarity 100.0%; Pred. No. 2.1e-148;
Matches 460; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDWTWRIFLVAAATGAHSEVQLVPGGSLRLSCAASGFTSDYMWVRAP 60
Db 1 MDWTWRIFLVAAATGAHSEVQLVPGGSLRLSCAASGFTSDYMWVRAP 60

QY 61 GKLEWVADIKNDGSYTNYAPSLTNRTTISRDNKNSLYLQMSLRAEDTAVYYCARELT 120
DB 61 GKLEWVADIKNDGSYTNYAPSLTNRTTISRDNKNSLYLQMSLRAEDTAVYYCARELT 120
QY 121 GTWQGTMTVTSASTKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALT 180
DB 121 GTWQGTMTVTSASTKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALT 180
QY 181 SGVHTTFAVLQSSGLYSLSVWTVPSSTLTGTYTCNVDPKPSNTKVDKRVESKYGPPCP 240
DB 181 SGVHTTFAVLQSSGLYSLSVWTVPSSTLTGTYTCNVDPKPSNTKVDKRVESKYGPPCP 240
QY 241 PCPAPFLGSPSVFLPAPKPTLMISRTPEVTCVVDVDSQEDPEVQFNWYDGVVEVNA 300
DB 241 PCPAPFLGSPSVFLPAPKPTLMISRTPEVTCVVDVDSQEDPEVQFNWYDGVVEVNA 300
QY 301 KTKPREEQNSTYRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIKAKGQPREPQ 360
DB 301 KTKPREEQNSTYRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIKAKGQPREPQ 360
QY 361 VYTLPPSQEEMTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY 420
DB 361 VYTLPPSQEEMTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY 420
QY 421 SRLTVDKSRWQEGNVFSCSVNHEALHNHYTQKSLSLGLK 460
DB 421 SRLTVDKSRWQEGNVFSCSVNHEALHNHYTQKSLSLGLK 460

RESULT 2

US-10-663-244-163
; Sequence 163, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; PRIOR FILING DATE: 2003-09-15
; PRIOR FILING DATE: 2002-09-13
; PRIOR FILING DATE: 2002-09-13
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 163
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-163

Query Match 92.5%; Score 2269; DB 16; Length 462;
Best Local Similarity 93.1%; Pred. No. 1.3e-136;
Matches 433; Conservative 7; Mismatches 17; Indels 8; Gaps 2;
QY 1 MDWTRILFLVAATGAHSEVQLVESGGGLVQPGGSLRLSCAASGFTFSDYMWVROAP 60
DB 1 MGWSCIILFLVATATGAHSEVQLVESGGGLVQPGGSLRLSCAASGFTFYNGWVROAP 60
QY 61 GKLEWVADIKNDGSYTNYAPSLTNRTTISRDNKNSLYLQMSLRAEDTAVYYCARELT 120
DB 61 GKLEWVADIKNDGSYTNYAPSLTNRTTISRDNKNSLYLQMSLRAEDTAVYYCARELT 120
QY 121 GT-----WGQGTMTVTSASTKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPTVTSW 175
DB 118 GTRVTWNGQTLTVTSASTKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPTVTSW 177
QY 176 SGALTSGVHTTFAVLQSSGLYSLSVWTVPSSTLTGTYTCNVDPKPSNTKVDKRVESKY 235

DB 178 SGALTSGVHTTFAVLQSSGLYSLSVWTVPSSTLTGTYTCNVDPKPSNTKVDKRVESKY 237
QY 236 GPCCPAPFLGSPSVFLPAPKPTLMISRTPEVTCVVDVDSQEDPEVQFNWYDGV 295
DB 238 GPCCPAPFLGSPSVFLPAPKPTLMISRTPEVTCVVDVDSQEDPEVQFNWYDGV 297
QY 296 EVNNAKTPREEQNSTYRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIKAKGQ 355
DB 298 EVNNAKTPREEQNSTYRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIKAKGQ 357
QY 356 PRPQVYTLPPSQEEMTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPVLDSDG 415
DB 358 PRPQVYTLPPSQEEMTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPVLDSDG 417
QY 416 SFPLYSLRTVDKSRWQEGNVFSCSVNHEALHNHYTQKSLSLGLK 460
DB 418 SFPLYSLRTVDKSRWQEGNVFSCSVNHEALHNHYTQKSLSLGLK 462

RESULT 3

US-10-663-244-160
; Sequence 160, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; PRIOR FILING DATE: 2003-09-15
; PRIOR FILING DATE: 2002-09-13
; PRIOR FILING DATE: 2002-09-13
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 160
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-160

Query Match 92.4%; Score 2268.5; DB 16; Length 463;
Best Local Similarity 92.7%; Pred. No. 1.4e-136;
Matches 429; Conservative 12; Mismatches 19; Indels 3; Gaps 1;
QY 1 MDWTRILFLVAATGAHSEVQLVESGGGLVQPGGSLRLSCAASGFTFSDYMWVROAP 60
DB 1 MGWSCIILFLVATATGAHSEVQLVESGGGLVQPGGSLRLSCAASGFTFSDYMWVROAP 60
QY 61 GKLEWVADIKNDGSYTNYAPSLTNRTTISRDNKNSLYLQMSLRAEDTAVYYCAR--- 117
DB 61 GKLEWVADIKNDGSYTNYAPSLTNRTTISRDNKNSLYLQMSLRAEDTAVYYCAR 120
QY 118 ELTGWQGTMTVTSASTKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSG 177
DB 121 SQPAIWQGGSLTVTSASTKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSG 180
QY 178 ALTGSGVHTTFAVLQSSGLYSLSVWTVPSSTLTGTYTCNVDPKPSNTKVDKRVESKYGP 237
DB 181 ALTGSGVHTTFAVLQSSGLYSLSVWTVPSSTLTGTYTCNVDPKPSNTKVDKRVESKYGP 240
QY 238 PCPCPAPFLGSPSVFLPAPKPTLMISRTPEVTCVVDVDSQEDPEVQFNWYDGV 297
DB 241 PCPCPAPFLGSPSVFLPAPKPTLMISRTPEVTCVVDVDSQEDPEVQFNWYDGV 300
QY 298 HNAKTPREEQNSTYRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIKAKGQPR 357
DB 301 HNAKTPREEQNSTYRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIKAKGQPR 360